bio-protocol Preprint

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Processing of single-cell data

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An abbreviated version of this protocol was published in eLIFE in Aug 2019

Testis single-cell RNA-seq reveals the dynamics of de novo gene transcription and germline mutational bias in *Drosophila*

DOI: 10.7554/eLife.47138

Detailed protocol

Hello,
When we ran cellranger count, we used --force-cells=5000. Cellranger then takes the 5000 "cells" with the most UMIs. We did this because testis cells vary heavily in RNA content, so we were forced to assume that our output has 5000 cells instead of relying on Cellranger's decision of what a cell is.
-Evan Witt

How to cite:(Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Witt, E. (2020). Processing of single-cell data. Bio-protocol Preprint. bio-protocol.org/prep377.
2. Witt, E., Benjamin, S., Svetec, N. and Zhao, L.(2019). Testis single-cell RNA-seq reveals the dynamics of de novo gene transcription and germline mutational bias in *Drosophila*. eLIFE. DOI: 10.7554/eLife.47138

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